CLAIMS

1. A protein crystal comprising the processivity clamp factor of DNA polymerase and a peptide of about 3 to about 30 amino acids, in particular of about 16 amino acids, said peptide comprising all or part of the processivity clamp factor binding sequence of a processivity clamp factor interacting protein, such as prokaryotic Pol I, Pol II, Pol III, Pol IV, Pol V, MutS, ligase I, α subunit of DNA polymerase, UmuD or UmuD', or eukaryotic pol ε, pol δ, pol η, pol ι, pol κ.

2. A protein crystal according to claim 1, wherein the processivity clamp factor of DNA polymerase is the β subunit of DNA polymerase, in particular the β subunit of DNA polymerase III of *Escherichia coli*, and the peptide has the following sequence:

VTLLDPQMERQLVLGL (SEQ ID NO: 1)

3. A protein crystal according to claim 1 or 2, comprising the β subunit of DNA polymerase III of *Escherichia coli* and the peptide of SEQ ID NO: 1, said crystal being triclinic and its cell dimensions being approximately a = 41.23 Å, b = 65.22 Å, c = 73.38 Å, α = 73.11°, β = 85.58°, γ = 85.80°.

4. A protein crystal according to claim 3, characterized by the atomic coordinates such as obtained by the X-ray diffraction of said crystal, said atomic coordinates being represented in Figure 1.

5. A protein crystal according to claim 3 or 4, characterized by the atomic coordinates representing the peptide and the peptide binding site of the β subunit of DNA polymerase III of *Escherichia coli*, and being as follows:

ATOM	4045	N	LEU	B	155	5.874	17.816	22.109	1.00	1.00	B
ATOM	4046	CA	LEU	B	155	6.029	16.359	22.087	1.00	1.00	B
ATOM	4047	CB	LEU	B	155	5.055	15.686	23.064	1.00	1.00	B
ATOM	4048	CG	LEU	B	155	5.260	16.046	24.536	1.00	1.00	B
ATOM	4049	CD1	LEU	B	155	4.256	15.237	25.360	1.00	1.00	B
ATOM	4050	CD2	LEU	B	155	6.686	15.757	24.980	1.00	1.00	B
ATOM	4051	C	LEU	B	155	5.808	15.776	20.682	1.00	1.00	B
ATOM	4052	O	LEU	B	155	6.177	14.613	20.431	1.00	1.00	B
ATOM	4177	N	THR	B	172	9.112	11.246	22.902	1.00	1.00	B
ATOM	4178	CA	THR	B	172	8.212	10.730	23.917	1.00	1.00	B
ATOM	4179	CB	THR	B	172	8.776	11.014	25.344	1.00	1.00	B
ATOM	4180	OG1	THR	B	172	7.931	10.400	26.328	1.00	1.00	B
ATOM	4181	CG2	THR	B	172	8.870	12.532	25.619	1.00	1.00	B
ATOM	4182	C	THR	B	172	6.805	11.269	23.709	1.00	1.00	B
ATOM	4183	O	THR	B	172	6.588	12.352	23.145	1.00	1.00	B
ATOM	4192	N	GLY	B	174	4.562	10.770	26.397	1.00	1.00	B

ATOM	4193	CA	GLY	B	174	3.992	10.745	27.737	1.00	1.00	B
ATOM	4194	C	GLY	B	174	3.762	9.337	28.266	1.00	1.00	B
ATOM	4195	O	GLY	B	174	3.667	9.141	29.489	1.00	1.00	B
ATOM	4196	N	HIS	B	175	3.650	8.349	27.375	1.00	1.00	B
ATOM	4197	CA	HIS	B	175	3.440	6.953	27.796	1.00	1.00	B
ATOM	4198	CB	HIS	B	175	2.313	6.309	26.977	1.00	1.00	B
ATOM	4199	CG	HIS	B	175	0.992	6.997	27.119	1.00	1.00	B
ATOM	4200	CD2	HIS	B	175	0.106	7.435	26.193	1.00	1.00	B
ATOM	4201	ND1	HIS	B	175	0.420	7.255	28.345	1.00	1.00	B
ATOM	4202	CE1	HIS	B	175	-0.763	7.817	28.170	1.00	1.00	B
ATOM	4203	NE2	HIS	B	175	-0.977	7.938	26.875	1.00	1.00	B
ATOM	4204	C	HIS	B	175	4.706	6.135	27.641	1.00	1.00	B
ATOM	4205	O	HIS	B	175	4.990	5.212	28.403	1.00	1.00	B
ATOM	4206	N	ARG	B	176	5.481	6.461	26.617	1.00	18.76	B
ATOM	4207	CA	ARG	B	176	6.711	5.768	26.422	1.00	18.30	B
ATOM	4208	CB	ARG	B	176	6.575	4.633	25.398	1.00	19.53	B
ATOM	4209	CG	ARG	B	176	6.329	5.094	23.954	1.00	22.88	B
ATOM	4210	CD	ARG	B	176	4.876	4.888	23.657	1.00	22.11	B
ATOM	4211	NE	ARG	B	176	4.435	5.312	22.314	1.00	22.09	B
ATOM	4212	CZ	ARG	B	176	4.555	4.591	21.202	1.00	20.17	B
ATOM	4213	NH1	ARG	B	176	5.159	3.403	21.213	1.00	17.04	B
ATOM	4214	NH2	ARG	B	176	3.914	4.977	20.120	1.00	20.02	B
ATOM	4215	C	ARG	B	176	7.684	6.807	25.902	1.00	17.30	B
ATOM	4216	O	ARG	B	176	7.255	7.860	25.374	1.00	18.10	B
ATOM	4217	N	LEU	B	177	8.957	6.504	26.080	1.00	17.97	B
ATOM	4218	CA	LEU	B	177	10.049	7.360	25.633	1.00	17.85	B
ATOM	4219	CB	LEU	B	177	10.664	8.095	26.827	1.00	18.29	B
ATOM	4220	CG	LEU	B	177	11.921	8.955	26.611	1.00	16.28	B
ATOM	4221	CD1	LEU	B	177	11.819	10.163	27.559	1.00	19.52	B
ATOM	4222	CD2	LEU	B	177	13.191	8.172	26.839	1.00	19.12	B
ATOM	4223	C	LEU	B	177	11.110	6.517	24.964	1.00	18.45	B
ATOM	4224	O	LEU	B	177	11.291	5.329	25.281	1.00	18.33	B
ATOM	4710	N	PRO	B	242	11.254	17.279	27.890	1.00	1.00	B
ATOM	4711	CD	PRO	B	242	9.987	16.826	27.286	1.00	1.00	B
ATOM	4712	CA	PRO	B	242	11.660	16.404	28.997	1.00	1.00	B
ATOM	4713	CB	PRO	B	242	10.688	15.230	28.874	1.00	1.00	B
ATOM	4714	CG	PRO	B	242	9.448	15.869	28.336	1.00	1.00	B
ATOM	4715	C	PRO	B	242	13.124	15.947	28.987	1.00	1.00	B
ATOM	4716	O	PRO	B	242	13.728	15.748	27.925	1.00	1.00	B
ATOM	4748	N	ARG	B	246	16.133	11.840	33.560	1.00	1.00	B
ATOM	4749	CA	ARG	B	246	15.239	11.808	34.707	1.00	1.00	B
ATOM	4750	CB	ARG	B	246	14.755	13.227	34.984	1.00	1.00	B
ATOM	4751	CG	ARG	B	246	15.880	14.252	35.113	1.00	1.00	B
ATOM	4752	CD	ARG	B	246	16.443	14.295	36.529	1.00	1.00	B
ATOM	4753	NE	ARG	B	246	15.374	14.318	37.524	1.00	1.00	B
ATOM	4754	CZ	ARG	B	246	14.316	15.126	37.477	1.00	1.00	B
ATOM	4755	NH1	ARG	B	246	14.169	15.992	36.481	1.00	1.00	B
ATOM	4756	NH2	ARG	B	246	13.396	15.067	38.430	1.00	1.00	B
ATOM	4757	C	ARG	B	246	14.022	10.889	34.566	1.00	1.00	B
ATOM	4758	O	ARG	B	246	13.384	10.536	35.560	1.00	1.00	B
ATOM	4759	N	VAL	B	247	13.695	10.532	33.327	1.00	1.00	B
ATOM	4760	CA	VAL	B	247	12.553	9.675	33.018	1.00	1.00	B
ATOM	4761	CB	VAL	B	247	12.061	9.942	31.585	1.00	1.00	B
ATOM	4762	CG1	VAL	B	247	10.930	8.991	31.216	1.00	1.00	B
ATOM	4763	CG2	VAL	B	247	11.624	11.391	31.462	1.00	1.00	B
ATOM	4764	C	VAL	B	247	12.962	8.218	33.133	1.00	1.00	B
ATOM	4765	O	VAL	B	247	12.125	7.334	33.308	1.00	1.00	B
ATOM	4996	N	PHE	B	278	-7.702	-1.352	24.244	1.00	1.00	B
ATOM	4997	CA	PHE	B	278	-6.698	-1.155	25.300	1.00	1.00	B
ATOM	4998	CB	PHE	B	278	-7.318	-1.432	26.663	1.00	1.00	B
ATOM	4999	CG	PHE	B	278	-8.431	-0.459	27.021	1.00	1.00	B
ATOM	5000	CD1	PHE	B	278	-8.142	0.882	27.268	1.00	1.00	B
ATOM	5001	CD2	PHE	B	278	-9.760	-0.869	27.021	1.00	1.00	B
ATOM	5002	CE1	PHE	B	278	-9.177	1.816	27.508	1.00	1.00	B
ATOM	5003	CE2	PHE	B	278	-10.795	0.052	27.258	1.00	1.00	B
ATOM	5004	CZ	PHE	B	278	-10.496	1.391	27.500	1.00	1.00	B
ATOM	5005	C	PHE	B	278	-5.403	-1.957	25.131	1.00	1.00	B
ATOM	5006	O	PHE	B	278	-4.356	-1.582	25.677	1.00	1.00	B
ATOM	5332	N	ASN	B	320	0.635	-2.143	27.431	1.00	1.00	B
ATOM	5333	CA	ASN	B	320	-0.051	-1.983	26.158	1.00	1.00	B
ATOM	5334	CB	ASN	B	320	-0.055	-0.504	25.796	1.00	1.00	B
ATOM	5335	CG	ASN	B	320	-0.561	-0.259	24.407	1.00	1.00	B
ATOM	5336	OD1	ASN	B	320	-0.226	-0.997	23.481	1.00	1.00	B
ATOM	5337	ND2	ASN	B	320	-1.362	0.791	24.242	1.00	1.00	B
ATOM	5338	C	ASN	B	320	0.927	-2.745	25.249	1.00	1.00	B
ATOM	5339	O	ASN	B	320	2.093	-2.350	25.102	1.00	1.00	B
ATOM	5353	N	TYR	B	323	2.932	-0.853	22.482	1.00	1.00	B

ATOM	5354	CA	TYR	B	323	4.110	-0.088	22.908	1.00	1.00	B
ATOM	5355	CB	TYR	B	323	3.878	0.590	24.259	1.00	1.00	B
ATOM	5356	CG	TYR	B	323	2.813	1.668	24.294	1.00	1.00	B
ATOM	5357	CD1	TYR	B	323	2.397	2.314	23.127	1.00	1.00	B
ATOM	5358	CE1	TYR	B	323	1.458	3.374	23.170	1.00	1.00	B
ATOM	5359	CD2	TYR	B	323	2.284	2.093	25.509	1.00	1.00	B
ATOM	5360	CE2	TYR	B	323	1.354	3.166	25.567	1.00	1.00	B
ATOM	5361	CZ	TYR	B	323	0.957	3.790	24.399	1.00	1.00	B
ATOM	5362	OH	TYR	B	323	0.112	4.886	24.453	1.00	1.00	B
ATOM	5363	C	TYR	B	323	5.327	-1.018	23.041	1.00	1.00	B
ATOM	5364	O	TYR	B	323	6.468	-0.646	22.726	1.00	1.00	B
ATOM	5519	N	VAL	B	344	3.837	-1.100	39.291	1.00	1.00	B
ATOM	5520	CA	VAL	B	344	3.324	0.227	39.030	1.00	1.00	B
ATOM	5521	CB	VAL	B	344	2.676	0.818	40.318	1.00	1.00	B
ATOM	5522	CG1	VAL	B	344	1.474	-0.026	40.725	1.00	1.00	B
ATOM	5523	CG2	VAL	B	344	3.687	0.847	41.456	1.00	1.00	B
ATOM	5524	C	VAL	B	344	4.405	1.163	38.512	1.00	1.00	B
ATOM	5525	O	VAL	B	344	4.199	2.365	38.405	1.00	1.00	B
ATOM	5532	N	SER	B	346	7.618	2.153	35.615	1.00	21.53	B
ATOM	5533	CA	SER	B	346	8.060	2.002	34.239	1.00	21.50	B
ATOM	5534	CB	SER	B	346	8.655	3.320	33.722	1.00	21.47	B
ATOM	5535	OG	SER	B	346	9.793	3.703	34.474	1.00	26.08	B
ATOM	5536	C	SER	B	346	9.107	0.914	34.106	1.00	20.70	B
ATOM	5537	O	SER	B	346	9.755	0.521	35.078	1.00	21.55	B
ATOM	5632	N	VAL	B	360	11.730	3.546	27.545	1.00	1.00	B
ATOM	5633	CA	VAL	B	360	11.023	3.501	28.812	1.00	1.00	B
ATOM	5634	CB	VAL	B	360	11.276	4.794	29.641	1.00	1.00	B
ATOM	5635	CG1	VAL	B	360	10.448	4.742	30.934	1.00	1.00	B
ATOM	5636	CG2	VAL	B	360	12.753	4.923	29.937	1.00	1.00	B
ATOM	5637	C	VAL	B	360	9.562	3.381	28.501	1.00	1.00	B
ATOM	5638	O	VAL	B	360	9.008	4.188	27.753	1.00	1.00	B
ATOM	5639	N	VAL	B	361	8.905	2.372	29.069	1.00	19.72	B
ATOM	5640	CA	VAL	B	361	7.488	2.188	28.831	1.00	18.92	B
ATOM	5641	CB	VAL	B	361	7.216	0.872	28.069	1.00	18.99	B
ATOM	5642	CG1	VAL	B	361	5.743	0.769	27.716	1.00	18.31	B
ATOM	5643	CG2	VAL	B	361	8.065	0.839	26.786	1.00	17.76	B
ATOM	5644	C	VAL	B	361	6.793	2.100	30.167	1.00	19.47	B
ATOM	5645	O	VAL	B	361	7.232	1.362	31.038	1.00	16.90	B
ATOM	5646	N	MET	B	362	5.737	2.885	30.318	1.00	1.00	B
ATOM	5647	CA	MET	B	362	4.962	2.882	31.540	1.00	1.00	B
ATOM	5648	CB	MET	B	362	4.226	4.206	31.682	1.00	1.00	B
ATOM	5649	CG	MET	B	362	3.918	4.589	33.122	1.00	1.00	B
ATOM	5650	SD	MET	B	362	5.405	4.806	34.163	1.00	1.00	B
ATOM	5651	CE	MET	B	362	4.575	4.880	35.731	1.00	1.00	B
ATOM	5652	C	MET	B	362	3.949	1.731	31.471	1.00	1.00	B
ATOM	5653	O	MET	B	362	3.385	1.438	30.410	1.00	1.00	B
ATOM	5654	N	PRO	B	363	3.698	1.069	32.599	1.00	1.00	B
ATOM	5655	CD	PRO	B	363	4.521	1.025	33.818	1.00	1.00	B
ATOM	5656	CA	PRO	B	363	2.729	-0.038	32.579	1.00	1.00	B
ATOM	5657	CB	PRO	B	363	3.155	-0.883	33.776	1.00	1.00	B
ATOM	5658	CG	PRO	B	363	3.665	0.160	34.754	1.00	1.00	B
ATOM	5659	C	PRO	B	363	1.272	0.395	32.672	1.00	1.00	B
ATOM	5660	O	PRO	B	363	0.959	1.574	32.811	1.00	1.00	B
ATOM	5661	N	MET	B	364	0.368	-0.568	32.537	1.00	1.00	B
ATOM	5662	CA	MET	B	364	-1.037	-0.272	32.674	1.00	1.00	B
ATOM	5663	CB	MET	B	364	-1.780	-0.391	31.332	1.00	1.00	B
ATOM	5664	CG	MET	B	364	-1.636	-1.670	30.568	1.00	1.00	B
ATOM	5665	SD	MET	B	364	-2.386	-1.510	28.872	1.00	1.00	B
ATOM	5666	CE	MET	B	364	-4.155	-1.253	29.308	1.00	1.00	B
ATOM	5667	C	MET	B	364	-1.602	-1.218	33.725	1.00	1.00	B
ATOM	5668	O	MET	B	364	-0.999	-2.251	34.035	1.00	1.00	B
ATOM	5669	N	ARG	B	365	-2.732	-0.836	34.307	1.00	1.00	B
ATOM	5670	CA	ARG	B	365	-3.383	-1.655	35.324	1.00	1.00	B
ATOM	5671	CB	ARG	B	365	-4.029	-0.756	36.394	1.00	1.00	B
ATOM	5672	CG	ARG	B	365	-4.785	-1.490	37.505	1.00	1.00	B
ATOM	5673	CD	ARG	B	365	-3.859	-2.316	38.398	1.00	1.00	B
ATOM	5674	NE	ARG	B	365	-4.571	-2.956	39.505	1.00	1.00	B
ATOM	5675	CZ	ARG	B	365	-3.984	-3.707	40.434	1.00	1.00	B
ATOM	5676	NH1	ARG	B	365	-2.678	-3.913	40.385	1.00	1.00	B
ATOM	5677	NH2	ARG	B	365	-4.698	-4.247	41.418	1.00	1.00	B
ATOM	5678	C	ARG	B	365	-4.459	-2.492	34.648	1.00	1.00	B
ATOM	5679	O	ARG	B	365	-5.449	-1.961	34.150	1.00	1.00	B
ATOM	5680	N	LEU	B	366	-4.267	-3.801	34.609	1.00	41.59	B
ATOM	5681	CA	LEU	B	366	-5.272	-4.665	33.996	1.00	44.25	B
ATOM	5682	CB	LEU	B	366	-4.615	-5.908	33.366	1.00	45.24	B
ATOM	5683	CG	LEU	B	366	-3.640	-5.701	32.202	1.00	45.46	B
ATOM	5684	CD1	LEU	B	366	-4.331	-5.029	31.031	1.00	47.09	B

ATOM	5685	CD2	LEU	B	366	-2.489	-4.856	32.678	1.00	46.71	B
ATOM	5686	C	LEU	B	366	-6.263	-5.080	35.092	1.00	45.55	B
ATOM	5687	O	LEU	B	366	-6.424	-6.296	35.333	1.00	46.32	B
ATOM	5688	OXT	LEU	B	366	-6.868	-4.169	35.704	1.00	46.33	B
ATOM	5689	CB	ARG	C	10	-5.663	0.205	32.737	0.76	1.00	C
ATOM	5690	CG	ARG	C	10	-7.073	-0.397	32.771	0.76	1.00	C
ATOM	5691	CD	ARG	C	10	-7.748	-0.383	31.408	0.76	1.00	C
ATOM	5692	NE	ARG	C	10	-8.728	-1.462	31.268	0.76	1.00	C
ATOM	5693	CZ	ARG	C	10	-9.992	-1.301	30.875	0.76	1.00	C
ATOM	5694	NH1	ARG	C	10	-10.464	-0.093	30.582	0.76	1.00	C
ATOM	5695	NH2	ARG	C	10	-10.779	-2.365	30.749	0.76	1.00	C
ATOM	5696	C	ARG	C	10	-4.106	2.152	32.497	0.76	1.00	C
ATOM	5697	O	ARG	C	10	-3.278	1.863	33.369	0.76	1.00	C
ATOM	5698	N	ARG	C	10	-6.417	2.186	31.464	0.76	1.00	C
ATOM	5699	CA	ARG	C	10	-5.587	1.727	32.625	0.76	1.00	C
ATOM	5700	N	GLN	C	11	-3.805	2.853	31.408	0.76	1.00	C
ATOM	5701	CA	GLN	C	11	-2.458	3.321	31.094	0.76	1.00	C
ATOM	5702	CB	GLN	C	11	-2.423	3.866	29.662	0.76	1.00	C
ATOM	5703	CG	GLN	C	11	-1.047	4.361	29.231	0.76	1.00	C
ATOM	5704	CD	GLN	C	11	-0.039	3.245	29.174	0.76	1.00	C
ATOM	5705	OE1	GLN	C	11	-0.263	2.232	28.494	0.76	1.00	C
ATOM	5706	NE2	GLN	C	11	1.082	3.415	29.876	0.76	1.00	C
ATOM	5707	C	GLN	C	11	-1.895	4.396	32.038	0.76	1.00	C
ATOM	5708	O	GLN	C	11	-2.494	5.467	32.217	0.76	1.00	C
ATOM	5709	N	LEU	C	12	-0.732	4.111	32.618	0.76	1.00	C
ATOM	5710	CA	LEU	C	12	-0.065	5.046	33.519	0.76	1.00	C
ATOM	5711	CB	LEU	C	12	0.754	4.277	34.561	0.76	1.00	C
ATOM	5712	CG	LEU	C	12	-0.036	3.305	35.450	0.76	1.00	C
ATOM	5713	CD1	LEU	C	12	0.907	2.681	36.468	0.76	1.00	C
ATOM	5714	CD2	LEU	C	12	-1.184	4.040	36.153	0.76	1.00	C
ATOM	5715	C	LEU	C	12	0.845	5.948	32.680	0.76	1.00	C
ATOM	5716	O	LEU	C	12	1.111	5.653	31.510	0.76	1.00	C
ATOM	5717	N	VAL	C	13	1.317	7.044	33.273	0.76	1.00	C
ATOM	5718	CA	VAL	C	13	2.166	7.987	32.543	0.76	1.00	C
ATOM	5719	CB	VAL	C	13	1.473	9.371	32.386	0.76	1.00	C
ATOM	5720	CG1	VAL	C	13	0.217	9.239	31.523	0.76	1.00	C
ATOM	5721	CG2	VAL	C	13	1.113	9.929	33.750	0.76	1.00	C
ATOM	5722	C	VAL	C	13	3.542	8.211	33.174	0.76	1.00	C
ATOM	5723	O	VAL	C	13	3.740	8.050	34.381	0.76	1.00	C
ATOM	5724	N	LEU	C	14	4.498	8.596	32.339	0.76	1.00	C
ATOM	5725	CA	LEU	C	14	5.860	8.846	32.803	0.76	1.00	C
ATOM	5726	CB	LEU	C	14	6.836	8.819	31.619	0.76	1.00	C
ATOM	5727	CG	LEU	C	14	6.972	7.481	30.889	0.76	1.00	C
ATOM	5728	CD1	LEU	C	14	7.666	7.705	29.557	0.76	1.00	C
ATOM	5729	CD2	LEU	C	14	7.744	6.495	31.769	0.76	1.00	C
ATOM	5730	C	LEU	C	14	6.010	10.186	33.517	0.76	1.00	C
ATOM	5731	O	LEU	C	14	5.238	11.126	33.284	0.76	1.00	C
ATOM	5732	N	GLY	C	15	7.000	10.263	34.396	0.76	1.00	C
ATOM	5733	CA	GLY	C	15	7.264	11.510	35.090	0.76	1.00	C
ATOM	5734	C	GLY	C	15	8.263	12.275	34.234	0.76	1.00	C
ATOM	5735	O	GLY	C	15	9.472	12.210	34.462	0.76	1.00	C
ATOM	5736	N	LEU	C	16	7.750	12.995	33.241	0.76	1.00	C
ATOM	5737	CA	LEU	C	16	8.576	13.756	32.306	0.76	1.00	C
ATOM	5738	CB	LEU	C	16	7.732	14.157	31.094	0.76	1.00	C
ATOM	5739	CG	LEU	C	16	7.258	12.955	30.269	0.76	1.00	C
ATOM	5740	CD1	LEU	C	16	6.303	13.411	29.171	0.76	1.00	C
ATOM	5741	CD2	LEU	C	16	8.467	12.233	29.690	0.76	1.00	C
ATOM	5742	C	LEU	C	16	9.263	14.982	32.898	0.76	1.00	C
ATOM	5743	O	LEU	C	16	10.182	15.515	32.231	0.76	1.00	C
ATOM	5744	OXT	LEU	C	16	8.870	15.398	34.009	0.76	1.00	C
END											

wherein atoms 4045 to 5688 represent the peptide binding site and atoms 5689 to 5748 represent the peptide.

6. A method to obtain a protein crystal as defined in claims 1 to 5, comprising the following steps:

- mixing a solution of processivity clamp factor of DNA polymerase, with a solution of a peptide of about 3 to about 30 amino acids, in particular of

about 16 amino acids, said peptide comprising all or part of the processivity clamp factor binding sequence of a processivity clamp factor interacting protein, such as prokaryotic Pol I, Pol II, Pol III, Pol IV, Pol V, MutS, ligase I, α subunit of DNA polymerase, UmuD or UmuD', or eukaryotic pol ε, pol δ, pol η, pol ι, pol κ, and with a solution of MES pH 6.0 0.2 M, $CaCl_2$ 0.2 M, PEG 400 60%, to obtain a crystallisation drop,

- letting the crystallisation drop concentrate against a solution of MES pH 6.0 0.1 M, $CaCl_2$ 0.1 M, PEG 400 30%, by vapour diffusion, to obtain a protein crystal.

7. A method according to claim 6, wherein the processivity clamp factor of DNA polymerase is the β subunit of DNA polymerase, in particular the β subunit of DNA polymerase III of *Escherichia coli*, and the peptide has the following sequence:

VTLLDPQMERQLVLGL (SEQ ID NO: 1).

8. The use of the atomic coordinates as defined in claims 4 and 5, for the screening, the design or the modification of ligands of the processivity clamp factor of DNA polymerase, in particular of the β subunit of DNA polymerase, in particular the β subunit of DNA polymerase III of *Escherichia coli*.

9. The use according to claim 8, for the screening, the design or the modification of ligands liable to be used for the preparation of pharmaceutical compositions useful for the treatment of bacterial diseases or diseases originating from DNA synthesis processes, such as fragile X syndrome, or proliferative disorders, such as cancers.

10. A method to screen ligands of the processivity clamp factor of DNA polymerase, said method comprising the step of assessing the interaction of tridimensional models of the ligands to screen with the structure of the β subunit of DNA polymerase as defined by the atomic coordinates according to claim 4, and in particular with the structure of the peptide binding site as defined by the atomic coordinates according to claim 5, and more particularly with at least nine of the following amino acids: Leu 155, Thr 172, Gly 174, His 175, Arg 176, Leu 177, Pro 242,

Arg 246, Val 247, Phe 278, Asn 320, Tyr 323, Val 344, Ser 346, Val 360, Val 361, Met 362, Pro 363, Met 364, Arg 365, Leu 366.

11. A method according to claim 10, to screen ligands liable to be used for the preparation of pharmaceutical compositions useful for the treatment of bacterial diseases or diseases originating from DNA synthesis processes, such as fragile X syndrome, or proliferative disorders, such as cancers.

12. A method to design or to modify compounds liable to bind to the processivity clamp factor of DNA polymerase, said method comprising the step of designing or modifying a compound, so that the tridimensional model of said compound is liable to interact with the structure of the β subunit of DNA polymerase as defined by the atomic coordinates according to claim 4, and in particular with the structure of the peptide binding site as defined by the atomic coordinates according to claim 5, and more particularly with at least nine of the following amino acids: Leu 155, Thr 172, Gly 174, His 175, Arg 176, Leu 177, Pro 242, Arg 246, Val 247, Phe 278, Asn 320, Tyr 323, Val 344, Ser 346, Val 360, Val 361, Met 362, Pro 363, Met 364, Arg 365, Leu 366.

13. A method according to claim 12, to design or to modify ligands liable to be used for the preparation of pharmaceutical compositions useful for the treatment of bacterial diseases or diseases originating from DNA synthesis processes, such as fragile X syndrome, or proliferative disorders, such as cancers.

14. A peptide of the following sequence:

VTLLDPQMERQLVLGL (SEQ ID NO: 1).

15. A pharmaceutical composition comprising as active substance the peptide of claim 14 in association with a pharmaceutically acceptable carrier.

16. The use of the peptide of claim 14 as an anti-bacterial compound.

17. The use of the peptide of claim 14 for the manufacture of a medicament for the treatment of bacterial diseases or diseases originating from DNA synthesis processes, such as fragile X syndrome, or of proliferative disorders, such as cancers.

18. A method to test *in vitro* the inhibitory effect of compounds on the processivity clamp factor-dependant activity of DNA polymerase, in particular of Pol IV DNA polymerase of *Escherichia. coli*, or of the α subunit of Pol III DNA polymerase of *Escherichia coli*, comprising the following steps:

- adding to assay solutions comprising a labelled nucleotidic primer, a template DNA, and DNA polymerase, in particular Pol IV DNA polymerase of *Escherichia coli*, or the α subunit of Pol III DNA polymerase of *Escherichia coli*, a compound to test at a given concentration for each assay solution, in the presence or the absence of the processivity clamp factor of DNA polymerase, in particular the β subunit of DNA polymerase, in particular the β subunit of DNA polymerase III of *Escherichia coli*.

- electrophoretically migrating the abovementioned assay solutions,

- comparing the migration pattern of each assay solutions in the presence or the absence of the processivity clamp factor of DNA polymerase, in particular the β subunit of DNA polymerase, in particular the β subunit of DNA polymerase III of *Escherichia coli*.

19. The use of a method according to claim 18, for the screening of compounds liable to be used for the preparation of pharmaceutical compositions useful for the treatment of bacterial diseases or diseases originating from DNA synthesis processes, such as fragile X syndrome, or proliferative disorders, such as cancers.